

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hedrick, Joseph A.
Vicari, Alain P.
Zlotnik, Albert
- (ii) TITLE OF INVENTION: Mammalian Chemokines; Receptors;
Reagents; Uses
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 24-JUL-1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0757
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 18..179

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: US 60/053,693

(I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GT	TAA	ACC	CAC	ACT	AT	TTC	AT	G	CAA	AAG	GG	T	GTA	GGG	TTA	CTG	AGG	ACA	GTT		50
					Met	Gln	Lys	Gly	Val	Gly	Leu	Leu	Arg	Thr	Val						
					1					5											
CCC	TTG	GTA	CCT	TCA	GTC	TCT	GGT	CAG	ATT	GAC	CTT	TTG	GTA	CTG	TGT						98
Pro	Leu	Val	Pro	Ser	Val	Ser	Gly	Gln	Ile	Asp	Leu	Leu	Val	Leu	Cys						
			15					20						25							
ATG	TGT	ATA	AAA	ACG	ACT	ACT	CCT	CAT	ATA	TTT	ATT	TCT	GAT	TAT	AAG						146
Met	Cys	Ile	Lys	Thr	Thr	Thr	Pro	His	Ile	Phe	Ile	Ser	Asp	Tyr	Lys						
			30					35					40								
ATA	ATA	TAT	TCT	GGA	AAA	CAC	TGG	AAA	ATA	CAT											179
Ile	Ile	Tyr	Ser	Gly	Lys	His	Trp	Lys	Ile	His											
			45					50													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gln	Lys	Gly	Val	Gly	Leu	Leu	Arg	Thr	Val	Pro	Leu	Val	Pro	Ser						
1				5					10					15							
Val	Ser	Gly	Gln	Ile	Asp	Leu	Leu	Val	Leu	Cys	Met	Cys	Ile	Lys	Thr						
			20					25					30								
Thr	Thr	Pro	His	Ile	Phe	Ile	Ser	Asp	Tyr	Lys	Ile	Ile	Tyr	Ser	Gly						
			35					40					45								
Lys	His	Trp	Lys	Ile	His																
			50																		

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 179..1171

(x) PUBLICATION INFORMATION:
(H) DOCUMENT NUMBER: US 60/053,693
(I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCTAAAACA AAATACAACA TTTCTTAAAT ACACTGTTTC CAGAAAGAGC TATTTTAACA	60
GAAGCAACTC AAAGATATCC CTTCGACAGA AGTGAAGTG CTGAAAAATG CTCATCTCTC	120
ACACAGACTT TTGATGGACA GGAGTTTCTA AGTATCATGC CTACCAACAA GCTGTAAA	178
ATG ATC ACC CTG AAC AAT CAA GAT CAA CCT GTC CCT TTT AAC AGC TCA Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser	226
1 5 10 15	
CAT CCA GAT GAA TAC AAA ATT GCA GCC CTT GTC TTC TAT AGC TGT ATC His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile	274
20 25 30	
TTC ATA ATT GGA TTA TTT GTT AAC ATC ACT GCA TTA TGG GTT TTC AGT Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser	322
35 40 45	
TGT ACC ACC AAG AAG AGA ACC ACG GTA ACC ATC TAT ATG ATG AAT GTG Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val	370
50 55 60	
GCA TTA GTG GAC TTG ATA TTT ATA ATG ACT TTA CCC TTT CGA ATG TTT Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe	418
65 70 75 80	
TAT TAT GCA AAA GAT GCA TGG CCA TTT GGA GAG TAC TTC TGC CAG ATT Tyr Tyr Ala Lys Asp Ala Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile	466
85 90 95	
ATT GGA GCT CTC ACA GTG TTT TAC CCA AGC ATT GCT TTA TGG CTT CTT Ile Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu	514
100 105 110	
GCC TTT ATT AGT GCT GAC AGA TAC ATG GCC ATT GTA CAG CCG AAG TAC Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr	562
115 120 125	
GCC AAA GAA CTT AAA AAC ACG TGC AAA GCC GTG CTG GCG TGT GTG GGA Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly	610
130 135 140	
GTC TGG ATA ATG ACC CTG ACC ACG ACC ACC CCT CTG CTA CTG CTC TAT Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Leu Tyr	658
145 150 155 160	
AAA GAC CCA GAT AAA GAC TCC ACT CCC GCC ACC TGC CTC AAG ATT TCT Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser	706
165 170 175	

GAC ATC ATC TAT CTA AAA GCT GTG AAC GTG CTG AAC CTC ACT CGA CTG	754
Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu	
180 185 190	
ACA TTT TTT TTC TTG ATT CCT TTG TTC ATC ATG ATT GGG TGC TAC TTG	802
Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu	
195 200 205	
GTC ATT ATT CAT AAT CTC CTT CAC GGC AGG ACG TCT AAG CTG AAA CCC	850
Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro	
210 215 220	
AAA GTC AAG GAG AAG TCC ATA AGG ATC ATC ATC ACG CTG CTG GTG CAG	898
Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Thr Leu Leu Val Gln	
225 230 235 240	
GTG CTC GTC TGC TTT ATG CCC TTC CAC ATC TGT TTC GCT TTC CTG ATG	946
Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met	
245 250 255	
CTG GGA ACG GGG GAG AAC AGT TAC AAT CCC TGG GGA GCC TTT ACC ACC	994
Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr	
260 265 270	
TTC CTC ATG AAC CTC AGC ACG TGT CTG GAT GTG ATT CTC TAC TAC ATC	1042
Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile	
275 280 285	
GTT TCA AAA CAA TTT CAG GCT CGA GTC ATT AGT GTC ATG CTA TAC CGT	1090
Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg	
290 295 300	
AAT TAC CTT CGA AGC ATG CGC AGA AAA AGT TTC CGA TCT GGT AGT CTA	1138
Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu	
305 310 315 320	
CGG TCA CTA AGC AAT ATA AAC AGT GAA ATG TTA TGAATAATAA GGTTCCTTCA	1191
Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu	
325 330	
TTTCAATCCC ATCAAAATTC ACTTCACTAA CTACTCTGGC GTCAATGGAT ATTCTGTATA	1251
ATACTATCAA GTCCCTTTTC TCTTGAAAAA ATAAATTCAT TATCTTCATT TTAAAACTT	1311
AAA	1314

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ile Thr Leu Asn Asn Gln Asp Gln Pro Val Pro Phe Asn Ser Ser
 1 5 10 15
 His Pro Asp Glu Tyr Lys Ile Ala Ala Leu Val Phe Tyr Ser Cys Ile
 20 25 30
 Phe Ile Ile Gly Leu Phe Val Asn Ile Thr Ala Leu Trp Val Phe Ser
 35 40 45
 Cys Thr Thr Lys Lys Arg Thr Thr Val Thr Ile Tyr Met Met Asn Val
 50 55 60
 Ala Leu Val Asp Leu Ile Phe Ile Met Thr Leu Pro Phe Arg Met Phe
 65 70 75 80
 Tyr Tyr Ala Lys Asp Ala Trp Pro Phe Gly Glu Tyr Phe Cys Gln Ile
 85 90 95
 Ile Gly Ala Leu Thr Val Phe Tyr Pro Ser Ile Ala Leu Trp Leu Leu
 100 105 110
 Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile Val Gln Pro Lys Tyr
 115 120 125
 Ala Lys Glu Leu Lys Asn Thr Cys Lys Ala Val Leu Ala Cys Val Gly
 130 135 140
 Val Trp Ile Met Thr Leu Thr Thr Thr Thr Pro Leu Leu Leu Tyr
 145 150 155 160
 Lys Asp Pro Asp Lys Asp Ser Thr Pro Ala Thr Cys Leu Lys Ile Ser
 165 170 175
 Asp Ile Ile Tyr Leu Lys Ala Val Asn Val Leu Asn Leu Thr Arg Leu
 180 185 190
 Thr Phe Phe Phe Leu Ile Pro Leu Phe Ile Met Ile Gly Cys Tyr Leu
 195 200 205
 Val Ile Ile His Asn Leu Leu His Gly Arg Thr Ser Lys Leu Lys Pro
 210 215 220
 Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Ile Thr Leu Leu Val Gln
 225 230 235 240
 Val Leu Val Cys Phe Met Pro Phe His Ile Cys Phe Ala Phe Leu Met
 245 250 255
 Leu Gly Thr Gly Glu Asn Ser Tyr Asn Pro Trp Gly Ala Phe Thr Thr
 260 265 270
 Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Ile Leu Tyr Tyr Ile
 275 280 285
 Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
 290 295 300

Asn Tyr Leu Arg Ser Met Arg Arg Lys Ser Phe Arg Ser Gly Ser Leu
 305 310 315 320

Arg Ser Leu Ser Asn Ile Asn Ser Glu Met Leu
 325 330

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 2..226

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: US 60/053,693
 (I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

G CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG GGA GCC TTC ACC	46
Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp Gly Ala Phe Thr	
1 5 10 15	
ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA GTC CTC TAC TAC	94
Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Val Leu Tyr Tyr	
20 25 30	
ATC GTT TCC AAA CAG TTC CAG GCT CGA GTC ATC AGC GTC ATG CTG TAC	142
Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr	
35 40 45	
CGC AAT TAC CTT CGC AGT GTT CGC AGA AAA AGT GTC CGA TCG GGC AGT	190
Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val Arg Ser Gly Ser	
50 55 60	
TTA CGG TCA CTT AGC AAC ATG AAC AGT GAG ATG CTT TGAGTCAGAG	236
Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu	
65 70 75	
CAAGCTGCCA GTCTTCAGTC TCTTTAAAAT TCTTTTCCTA TCTACTTTTCG GGTGAACCAG	296
CATTCTACAC TATCCAGTCC CTTCTCTAAC AAAGAGAAAT AATAATGATG AACTTTAAAA	356
ACTTCTGCGG TATTCTGTGT ATTCTAGCCA CATGATTAAA AACT	400

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp Gly Ala Phe Thr Thr
 1              5              10              15
Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Val Leu Tyr Tyr Ile
          20              25              30
Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met Leu Tyr Arg
          35              40              45
Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val Arg Ser Gly Ser Leu
          50              55              60
Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu
          65              70              75
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1549 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 85..1134

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 661
(D) OTHER INFORMATION: /note= "residue 661 may be G or C;
actually found to be A"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1462
(D) OTHER INFORMATION: /note= ""residue 1462 may be G or
T""

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1473
(D) OTHER INFORMATION: /note= ""residue 1473 may be A or
C""

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1490

(D) OTHER INFORMATION: /note= ""residue 1490 may be A, C,
T, or G""

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1495

(D) OTHER INFORMATION: /note= ""residue 1495 may be A or
T""

(x) PUBLICATION INFORMATION:

(H) DOCUMENT NUMBER: US 60/053,693

(I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATTTCGGCTTA CTCACTATAG GGCTCGAGCG GCGCCCGGGC AGGTCAAGAC TGCTCCTCTC	60
TGCCGACTAC AACAGATTGG AGCC ATG GCT TTG GAA CAG AAC CAG TCA ACA	111
Met Ala Leu Glu Gln Asn Gln Ser Thr	
1 5	
GAT TAT TAT TAT GAG GAA AAT GAA ATG AAC GGC ACT TAT GAC TAC AGT	159
Asp Tyr Tyr Tyr Glu Glu Asn Glu Met Asn Gly Thr Tyr Asp Tyr Ser	
10 15 20 25	
CAA TAT GAA CTG ATC TGT ATC AAA GAA GAT GTC AGA GAA TTT GCA AAA	207
Gln Tyr Glu Leu Ile Cys Ile Lys Glu Asp Val Arg Glu Phe Ala Lys	
30 35 40	
GTT TTC CTC CCT GTA TTC CTC ACA ATA GTT TTC GTC ATT GGA CTT GCA	255
Val Phe Leu Pro Val Phe Leu Thr Ile Val Phe Val Ile Gly Leu Ala	
45 50 55	
GGC AAT TCC ATG GTA GTG GCA ATT TAT GCC TAT TAC AAG AAA CAG AGA	303
Gly Asn Ser Met Val Val Ala Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg	
60 65 70	
ACC AAA ACA GAT GTG TAC ATC CTG AAT TTG GCT GTA GCA GAT TTA CTC	351
Thr Lys Thr Asp Val Tyr Ile Leu Asn Leu Ala Val Ala Asp Leu Leu	
75 80 85	
CTT CTA TTC ACT CTG CCT TTT TGG GCT GTT AAT GCA GTT CAT GGG TGG	399
Leu Leu Phe Thr Leu Pro Phe Trp Ala Val Asn Ala Val His Gly Trp	
90 95 100 105	
GTT TTA GGG AAA ATA ATG TGC AAA ATA ACT TCA GCC TTG TAC ACA CTA	447
Val Leu Gly Lys Ile Met Cys Lys Ile Thr Ser Ala Leu Tyr Thr Leu	
110 115 120	
AAC TTT GTC TCT GGA ATG CAG TTT CTG GCT TGT ATC AGC ATA GAC AGA	495
Asn Phe Val Ser Gly Met Gln Phe Leu Ala Cys Ile Ser Ile Asp Arg	
125 130 135	
TAT GTG GCA GTA ACT AAA GTC CCC AGC CAA TCA GGA GTG GGA AAA CCA	543
Tyr Val Ala Val Thr Lys Val Pro Ser Gln Ser Gly Val Gly Lys Pro	
140 145 150	
TGC TGG ATC ATC TGT TCC TGT GTC TGG ATG GCT GCC ATC TTG CTG AGC	591

Cys Trp Ile Ile Cys Ser Cys Val Trp Met Ala Ala Ile Leu Leu Ser	
155 160 165	
ATA CCC CAG CTG GTT TTT TAT ACA GTA AAT GAC AAT GCT AGG TGC ATT	639
Ile Pro Gln Leu Val Phe Tyr Thr Val Asn Asp Asn Ala Arg Cys Ile	
170 175 180 185	
CCC ATT TTC CCC CGC TAC CTA AGA ACA TCA ATG AAA GCA TTG ATT CAA	687
Pro Ile Phe Pro Arg Tyr Leu Arg Thr Ser Met Lys Ala Leu Ile Gln	
190 195 200	
ATG CTA GAG ATC TGC ATT GGA TTT GTA GTA CCC TTT CTT ATT ATG GGG	735
Met Leu Glu Ile Cys Ile Gly Phe Val Val Pro Phe Leu Ile Met Gly	
205 210 215	
GTG TGC TAC TTT ATC ACA GCA AGG ACA CTC ATG AAG ATG CCA AAC ATT	783
Val Cys Tyr Phe Ile Thr Ala Arg Thr Leu Met Lys Met Pro Asn Ile	
220 225 230	
AAA ATA TCT CGA CCC CTA AAA GTT CTG CTC ACA GTC GTT ATA GTT TTC	831
Lys Ile Ser Arg Pro Leu Lys Val Leu Leu Thr Val Val Ile Val Phe	
235 240 245	
ATT GTC ACT CAA CTG CCT TAT AAC ATT GTC AAG TTC TGC CGA GCC ATA	879
Ile Val Thr Gln Leu Pro Tyr Asn Ile Val Lys Phe Cys Arg Ala Ile	
250 255 260 265	
GAC ATC ATC TAC TCC CTG ATC ACC AGC TGC AAC ATG AGC AAA CGC ATG	927
Asp Ile Ile Tyr Ser Leu Ile Thr Ser Cys Asn Met Ser Lys Arg Met	
270 275 280	
GAC ATC GCC ATC CAA GTC ACA GAA AGC ATC GCA CTC TTT CAC AGC TGC	975
Asp Ile Ala Ile Gln Val Thr Glu Ser Ile Ala Leu Phe His Ser Cys	
285 290 295	
CTC AAC CCA ATC CTT TAT GTT TTT ATG GGA GCA TCT TTC AAA AAC TAC	1023
Leu Asn Pro Ile Leu Tyr Val Phe Met Gly Ala Ser Phe Lys Asn Tyr	
300 305 310	
GTT ATG AAA GTG GCC AAG AAA TAT GGG TCC TGG AGA AGA CAG AGA CAA	1071
Val Met Lys Val Ala Lys Lys Tyr Gly Ser Trp Arg Arg Gln Arg Gln	
315 320 325	
AGT GTG GAG GAG TTT CCT TTT GAT TCT GAG GGT CCT ACA GAG CCA ACC	1119
Ser Val Glu Glu Phe Pro Phe Asp Ser Glu Gly Pro Thr Glu Pro Thr	
330 335 340 345	
AGT ACT TTT AGC ATT TAAAGGTAAA ACTGCTCTGC CTTTGCTTG GATACATATG	1174
Ser Thr Phe Ser Ile	
350	
AATGATGCTT TCCCCTCAAA TAAACATCT GCATTATTCT GAAACTCAAA TCTCAGACGC	1234
CGTGGTTGCA ACTTATAATA AAGAATGGGT TGGGGGAAGG GGGAGAAATA AAAGCCAAGA	1294
AGAAGAAACA AGATAATAAA TGTACAAAAC ATGAAAATTA AAATGAACAA TATAGGAAAA	1354
TAATTGTAAC AGGCATAAGT GAATAACACT CTGCTGTAAC GAAGAAAAC TGTGGTGAT	1414

AATTTTGTAT CTTGGTTGCA GTGGTGCTTA TACCAATCTA CACCAGTGAT AAAATGACCC	1474
AGAACTATTT CCCCCCTTGT TCCCATTTC AATTCCTGGT TTTGACATTA TAGTATAATT	1534
ATGTTAGATG GAACC	1549

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Leu	Glu	Gln	Asn	Gln	Ser	Thr	Asp	Tyr	Tyr	Tyr	Glu	Glu	Asn	1	5	10	15
Glu	Met	Asn	Gly	Thr	Tyr	Asp	Tyr	Ser	Gln	Tyr	Glu	Leu	Ile	Cys	Ile	20	25	30	
Lys	Glu	Asp	Val	Arg	Glu	Phe	Ala	Lys	Val	Phe	Leu	Pro	Val	Phe	Leu	35	40	45	
Thr	Ile	Val	Phe	Val	Ile	Gly	Leu	Ala	Gly	Asn	Ser	Met	Val	Val	Ala	50	55	60	
Ile	Tyr	Ala	Tyr	Tyr	Lys	Lys	Gln	Arg	Thr	Lys	Thr	Asp	Val	Tyr	Ile	65	70	75	80
Leu	Asn	Leu	Ala	Val	Ala	Asp	Leu	Leu	Leu	Phe	Thr	Leu	Pro	Phe	85	90	95		
Trp	Ala	Val	Asn	Ala	Val	His	Gly	Trp	Val	Leu	Gly	Lys	Ile	Met	Cys	100	105	110	
Lys	Ile	Thr	Ser	Ala	Leu	Tyr	Thr	Leu	Asn	Phe	Val	Ser	Gly	Met	Gln	115	120	125	
Phe	Leu	Ala	Cys	Ile	Ser	Ile	Asp	Arg	Tyr	Val	Ala	Val	Thr	Lys	Val	130	135	140	
Pro	Ser	Gln	Ser	Gly	Val	Gly	Lys	Pro	Cys	Trp	Ile	Ile	Cys	Ser	Cys	145	150	155	160
Val	Trp	Met	Ala	Ala	Ile	Leu	Leu	Ser	Ile	Pro	Gln	Leu	Val	Phe	Tyr	165	170	175	
Thr	Val	Asn	Asp	Asn	Ala	Arg	Cys	Ile	Pro	Ile	Phe	Pro	Arg	Tyr	Leu	180	185	190	
Arg	Thr	Ser	Met	Lys	Ala	Leu	Ile	Gln	Met	Leu	Glu	Ile	Cys	Ile	Gly	195	200	205	

Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
 210 215 220
 Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
 225 230 235 240
 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
 245 250 255
 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
 260 265 270
 Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
 275 280 285
 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
 290 295 300
 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
 305 310 315 320
 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
 325 330 335
 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
 340 345 350

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 429..1238

(x) PUBLICATION INFORMATION:

- (H) DOCUMENT NUMBER: US 60/053,693
- (I) FILING DATE: 25-JUL-1997

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GATGCATGCT CGAGCGGCCG CCAGTGTGAT GGATATCTGC AGAATTCGGC TTACTCACTA	60
TAGGGCTCGA GCGGCCGCC GGGCAGGTCC CTCCAACAAG ACGCAGCACA GAGACACCAC	120
CTACCTAACA CAGGCGACTC TGAGCACTCT CTCTCTGGGA CTGGGCAGAG CGGCAAACGG	180
TCACCTCTCA GACAGCCTTT GACAGACAGG AGGTTCTACA TACCATGGGA GCCAGCCTGC	240
TGTAAGATGG CCACCCTGAG CAATCACAAC CAGCTTGATC TTTCTAATGG CTCACACCCA	300

GAGGAATACA AAATCGCAGC CCTAGTCTTC TACAGCTGCA TCTTCCTGAT TGGGCTGTTT	360
GTTAATGTCA CTGCGTTGTG GGTTTTCAGC TGTACGACCA AGAAAAGAAC ACAGTGACCA	420
TCTACATG ATG AAC GTT GCA CTA CTG GAC CTC GTA TTT ATA CTC AGT CTG Met Asn Val Ala Leu Leu Asp Leu Val Phe Ile Leu Ser Leu	470
1 5 10	
CCC TTT CGG ATG TTT TAC TAT GCA AAA GGC GAG TGG CCA TTT GGA GAG Pro Phe Arg Met Phe Tyr Tyr Ala Lys Gly Glu Trp Pro Phe Gly Glu	518
15 20 25 30	
TAC TTC TGC CAC ATT CTT GGG GCC CTG GTG GTG TTT TAC CCA AGC CTC Tyr Phe Cys His Ile Leu Gly Ala Leu Val Val Phe Tyr Pro Ser Leu	566
35 40 45	
GCT CTG TGG CTT CTT GCT TTC ATT AGT GCT GAC AGA TAC ATG GCC ATC Ala Leu Trp Leu Leu Ala Phe Ile Ser Ala Asp Arg Tyr Met Ala Ile	614
50 55 60	
GTA CAG CCA AAA TAT GCC AAG GAG CTG AAG AAC ACC GGC AAG GCC GTG Val Gln Pro Lys Tyr Ala Lys Glu Leu Lys Asn Thr Gly Lys Ala Val	662
65 70 75	
CTT GCG TGT GGG GGG GTC TGG GTA ATG ACC CTG ACC ACC ACT GTC CCC Leu Ala Cys Gly Gly Val Trp Val Met Thr Leu Thr Thr Thr Val Pro	710
80 85 90	
CTG CTA CTG CTC TAC GAA GAC CCA GAC AAT GCC TCC TCC CCG GCC ACC Leu Leu Leu Leu Tyr Glu Asp Pro Asp Asn Ala Ser Ser Pro Ala Thr	758
95 100 105 110	
TGC CTG AAG ATC TCC GAC ATC ACC CAC TTA AAA GCT GTC AAC GTG CTC Cys Leu Lys Ile Ser Asp Ile Thr His Leu Lys Ala Val Asn Val Leu	806
115 120 125	
AAC TTC ACG CGA CTC ATA TTT TTC TTC CTG ATC CCT TTG TTC ATC ATG Asn Phe Thr Arg Leu Ile Phe Phe Phe Leu Ile Pro Leu Phe Ile Met	854
130 135 140	
ATC GGG TGC TAC GTG GTC ATC ATT CAC AGT CTC CTC CGA GGG CAG ACG Ile Gly Cys Tyr Val Val Ile Ile His Ser Leu Leu Arg Gly Gln Thr	902
145 150 155	
TCT AAG CTG AAG CCC AAG GTC AAG GAG AAG TCC ATA CGG ATC ATC ATG Ser Lys Leu Lys Pro Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Met	950
160 165 170	
ACC CTC CTG CTG CAG GTG CTC GTC TGC TTC GTG CCC TTC CAC ATC TGC Thr Leu Leu Leu Gln Val Leu Val Cys Phe Val Pro Phe His Ile Cys	998
175 180 185 190	
TTT GCC GTC CTG ATG CTA CAA GGA CAG GAG AAC AGC TAT AGC CCC TGG Phe Ala Val Leu Met Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp	1046
195 200 205	
GGA GCC TTC ACC ACC TTC CTC ATG AAC CTC AGC ACC TGT CTC GAT GTA Gly Ala Phe Thr Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val	1094

210	215	220	
GTC CTC TAC TAC ATC GTT TCC AAA CAG TTC CAG GCT CGA GTC ATC AGC			1142
Val Leu Tyr Tyr Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser			
225	230	235	
GTC ATG CTG TAC CGC AAT TAC CTT CGC AGT GTT CGC AGA AAA AGT GTC			1190
Val Met Leu Tyr Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val			
240	245	250	
CGA TCG GGC AGT TTA CGG TCA CTT AGC AAC ATG AAC AGT GAG ATG CTT			1238
Arg Ser Gly Ser Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu			
255	260	265	270
TGAGTCAGAG CAAGCTGCCA GTCTTCAGTC TCTTT			1273

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asn	Val	Ala	Leu	Leu	Asp	Leu	Val	Phe	Ile	Leu	Ser	Leu	Pro	Phe
1				5					10					15	
Arg	Met	Phe	Tyr	Tyr	Ala	Lys	Gly	Glu	Trp	Pro	Phe	Gly	Glu	Tyr	Phe
			20					25					30		
Cys	His	Ile	Leu	Gly	Ala	Leu	Val	Val	Phe	Tyr	Pro	Ser	Leu	Ala	Leu
		35					40					45			
Trp	Leu	Leu	Ala	Phe	Ile	Ser	Ala	Asp	Arg	Tyr	Met	Ala	Ile	Val	Gln
	50					55					60				
Pro	Lys	Tyr	Ala	Lys	Glu	Leu	Lys	Asn	Thr	Gly	Lys	Ala	Val	Leu	Ala
	65				70					75				80	
Cys	Gly	Gly	Val	Trp	Val	Met	Thr	Leu	Thr	Thr	Thr	Val	Pro	Leu	Leu
			85						90					95	
Leu	Leu	Tyr	Glu	Asp	Pro	Asp	Asn	Ala	Ser	Ser	Pro	Ala	Thr	Cys	Leu
			100					105					110		
Lys	Ile	Ser	Asp	Ile	Thr	His	Leu	Lys	Ala	Val	Asn	Val	Leu	Asn	Phe
		115					120					125			
Thr	Arg	Leu	Ile	Phe	Phe	Phe	Leu	Ile	Pro	Leu	Phe	Ile	Met	Ile	Gly
	130					135					140				
Cys	Tyr	Val	Val	Ile	Ile	His	Ser	Leu	Leu	Arg	Gly	Gln	Thr	Ser	Lys
	145					150				155				160	

Leu Lys Pro Lys Val Lys Glu Lys Ser Ile Arg Ile Ile Met Thr Leu
165 170 175

Leu Leu Gln Val Leu Val Cys Phe Val Pro Phe His Ile Cys Phe Ala
180 185 190

Val Leu Met Leu Gln Gly Gln Glu Asn Ser Tyr Ser Pro Trp Gly Ala
195 200 205

Phe Thr Thr Phe Leu Met Asn Leu Ser Thr Cys Leu Asp Val Val Leu
210 215 220

Tyr Tyr Ile Val Ser Lys Gln Phe Gln Ala Arg Val Ile Ser Val Met
225 230 235 240

Leu Tyr Arg Asn Tyr Leu Arg Ser Val Arg Arg Lys Ser Val Arg Ser
245 250 255

Gly Ser Leu Arg Ser Leu Ser Asn Met Asn Ser Glu Met Leu
260 265 270